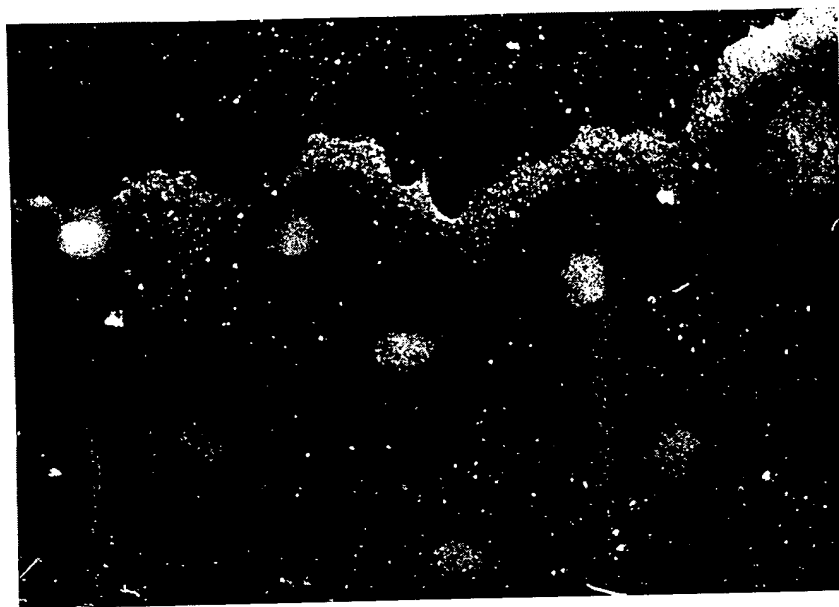


Figure 1



Bcap73 localizes to the forefront of endothelial cells migrating in response to injury.

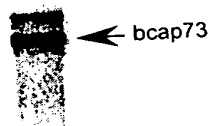
Figure 2



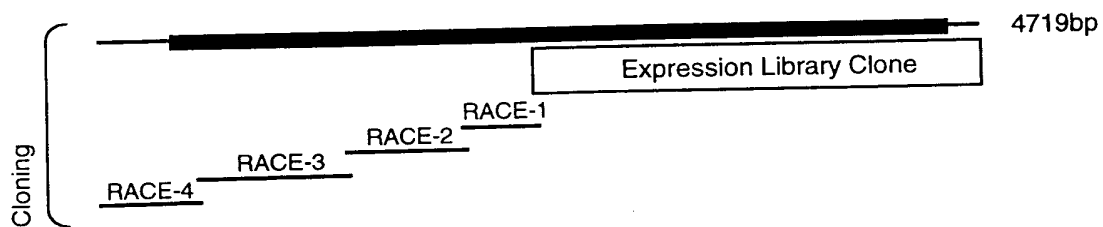
Bcap73 purification by ion-exchange chromatography.

Figure 3

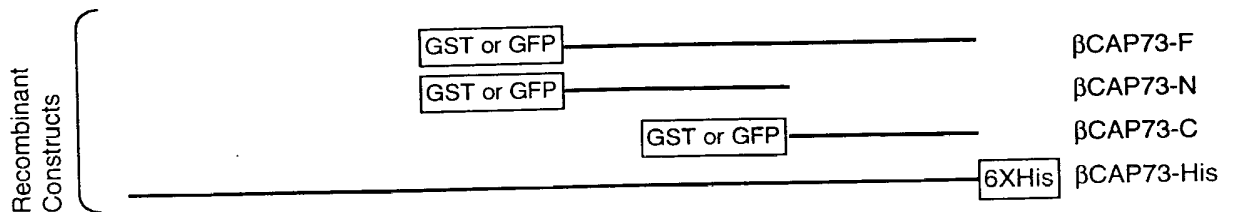
A



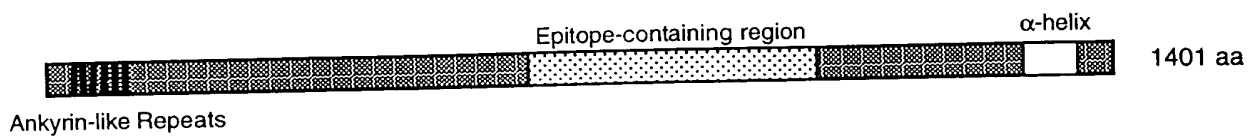
B



C



D



### Figure 4-1

1. *What is the purpose of the study?*  
 2. *What are the research questions or hypotheses?*  
 3. *What is the study design?*  
 4. *What are the participants and sample characteristics?*  
 5. *What are the independent and dependent variables?*  
 6. *What are the data collection methods?*  
 7. *What are the data analysis methods?*  
 8. *What are the results of the study?*  
 9. *What are the conclusions and implications of the study?*  
 10. *What are the limitations of the study?*  
 11. *What are the strengths of the study?*  
 12. *What are the future research directions?*  
 13. *What are the ethical considerations?*  
 14. *What are the funding sources?*  
 15. *What are the conflicts of interest?*  
 16. *What are the acknowledgments?*  
 17. *What are the references?*  
 18. *What are the appendices?*  
 19. *What are the footnotes?*  
 20. *What are the tables and figures?*  
 21. *What are the glossary and abbreviations?*  
 22. *What are the contact information and correspondence?*  
 23. *What are the permissions and approvals?*  
 24. *What are the disclosures and disclosures?*  
 25. *What are the disclosures and disclosures?*

Figure 4-2

gta gat ggg cgg aca cca ctt gtt ctg gct acc cag atg tgt agg cca	892
Val Asp Gly Arg Thr Pro Leu Val Leu Ala Thr Gln Met Cys Arg Pro	
155 160 165	
aca ata tgt caa ctg ctg ata gat aga ggg gcg gat att aat tcc aga	940
Thr Ile Cys Gln Leu Leu Ile Asp Arg Gly Ala Asp Ile Asn Ser Arg	
170 175 180	
gac aaa caa aac agg act gct ctc atg cta gga tgc gag tat ggt tgc	988
Asp Lys Gln Asn Arg Thr Ala Leu Met Leu Gly Cys Glu Tyr Gly Cys	
185 190 195	
aaa gat gca gta gaa gtc tta atc aaa aac ggc gct gac gtg acc ttg	1036
Lys Asp Ala Val Glu Val Leu Ile Lys Asn Gly Ala Asp Val Thr Leu	
200 205 210 215	
ctg gac gcc ctt ggc cat gac agt tct tac tat gca aga att ggt gac	1084
Leu Asp Ala Leu Gly His Asp Ser Ser Tyr Tyr Ala Arg Ile Gly Asp	
220 225 230	
aat ctg gac att cta acc tta ctg aag act gca tca gaa aat tcc aac	1132
Asn Leu Asp Ile Leu Thr Leu Leu Lys Thr Ala Ser Glu Asn Ser Asn	
235 240 245	
aaa ggg aga gaa ctt tgg aag aaa gga cca tct tta caa cag cga aat	1180
Lys Gly Arg Glu Leu Trp Lys Lys Gly Pro Ser Leu Gln Gln Arg Asn	
250 255 260	
ttg tct cag atg cta gat gaa gta aat acg aag tca aat cag agg gag	1228
Leu Ser Gln Met Leu Asp Glu Val Asn Thr Lys Ser Asn Gln Arg Glu	
265 270 275	
cat caa aac att cag gat ctg gag att gaa aat gaa gat ctg aaa gag	1276
His Gln Asn Ile Gln Asp Leu Glu Ile Glu Asn Glu Asp Leu Lys Glu	
280 285 290 295	
aga ttg aga aaa att cag caa gaa cag aga ata tta ttg gat aaa gtc	1324
Arg Leu Arg Lys Ile Gln Gln Glu Gln Arg Ile Leu Leu Asp Lys Val	
300 305 310	
aat ggt tta cag cta cag ctg aat gag gaa gta atg gtg gct gat gat	1372
Asn Gly Leu Gln Leu Gln Leu Asn Glu Glu Val Met Val Ala Asp Asp	
315 320 325	
ctg gaa agt gag aaa gaa aag ctg aag tcc ctt ttg gca gcc aaa gaa	1420
Leu Glu Ser Glu Lys Glu Lys Leu Lys Ser Leu Leu Ala Ala Lys Glu	
330 335 340	
aag cag cat gaa gaa agc cta aga act att gag gct ctg aaa agt aga	1468
Lys Gln His Glu Glu Ser Leu Arg Thr Ile Glu Ala Leu Lys Ser Arg	
345 350 355	

Figure 4-3

ttt aag tat ttt gag agt gat cat tta gga tca gga agt cat ttc agg	1516
Phe Lys Tyr Phe Glu Ser Asp His Leu Gly Ser Gly Ser His Phe Arg	
360 365 370 375	
aaa gaa gat atg ctt ctt aaa caa ggt caa atg tac atg aca gac tca	1564
Lys Glu Asp Met Leu Leu Lys Gln Gly Gln Met Tyr Met Thr Asp Ser	
380 385 390	
cag tgt act tcc aca ggc atg cca gtc cat atg caa agc cga tct atg	1612
Gln Cys Thr Ser Thr Gly Met Pro Val His Met Gln Ser Arg Ser Met	
395 400 405	
tta aga cca ctg gag cta gcc tta cct aat caa gcc tca tat tcg gaa	1660
Leu Arg Pro Leu Glu Leu Ala Leu Pro Asn Gln Ala Ser Tyr Ser Glu	
410 415 420	
aac gaa att tta aag aaa gaa tta gaa gca atg aga act ttc tgt gat	1708
Asn Glu Ile Leu Lys Lys Glu Leu Glu Ala Met Arg Thr Phe Cys Asp	
425 430 435	
tca gca aaa caa gac aga ctc aaa ctc caa aat gaa ctg gct cac aag	1756
Ser Ala Lys Gln Asp Arg Leu Lys Leu Gln Asn Glu Leu Ala His Lys	
440 445 450 455	
gtg gcg gag tgc aag gcc tta gca ttg gaa tgt gaa agg gtg aaa gag	1804
Val Ala Glu Cys Lys Ala Leu Ala Leu Glu Cys Glu Arg Val Lys Glu	
460 465 470	
gat tca gat gag cag ata aag caa cta gaa gat gcc ttg aaa gac gtg	1852
Asp Ser Asp Glu Gln Ile Lys Gln Leu Glu Asp Ala Leu Lys Asp Val	
475 480 485	
cag aag aga atg tat gag tcg gaa ggt aaa gtg aaa caa atg cag aca	1900
Gln Lys Arg Met Tyr Glu Ser Glu Gly Lys Val Lys Gln Met Gln Thr	
490 495 500	
cat ttt ctt gcc ttg aaa gag cac ctg aca agt gat gcg gcc act ggg	1948
His Phe Leu Ala Leu Lys Glu His Leu Thr Ser Asp Ala Ala Thr Gly	
505 510 515	
aac cac agg ctg atg gag gaa ctg aag gat cag ttg aaa gac atg aaa	1996
Asn His Arg Leu Met Glu Glu Leu Lys Asp Gln Leu Lys Asp Met Lys	
520 525 530 535	
gtg aaa tac gaa ggt gcg tcc gca gaa gtg ggg aaa ttg aga aac caa	2044
Val Lys Tyr Glu Gly Ala Ser Ala Glu Val Gly Lys Leu Arg Asn Gln	
540 545 550	
atc aaa caa aat gaa atg tta gtt gaa gag ttt aag aga gat gag ggc	2092
Ile Lys Gln Asn Glu Met Leu Val Glu Glu Phe Lys Arg Asp Glu Gly	
555 560 565	

Figure 4-4

aag ctg atg gaa gag aat aag cga ctg cag aag gag ttg agc atg tgt	2140
Lys Leu Met Glu Glu Asn Lys Arg Leu Gln Lys Glu Leu Ser Met Cys	
570 575 580	
gaa ctg gag cga gag aag aga gga agg aag ctc act gag atg gaa ggc	2188
Glu Leu Glu Arg Glu Lys Arg Gly Arg Lys Leu Thr Glu Met Glu Gly	
585 590 595	
cag tta aag gac ttg tca gcc aag ctg gcc ctt tct att cca gca gag	2236
Gln Leu Lys Asp Leu Ser Ala Lys Leu Ala Leu Ser Ile Pro Ala Glu	
600 605 610 615	
aaa ttt gaa aac atg aag agc ttg tta tca aat gaa ctg aac gag aag	2284
Lys Phe Glu Asn Met Lys Ser Leu Leu Ser Asn Glu Leu Asn Glu Lys	
620 625 630	
gca aaa aaa tta ata gat gtg gaa aga gaa tat gaa aga tca ctt aat	2332
Ala Lys Lys Leu Ile Asp Val Glu Arg Glu Tyr Glu Arg Ser Leu Asn	
635 640 645	
gaa act aga cca tta aag aga gaa ctt gag aat ttg aag gcc aaa ctg	2380
Glu Thr Arg Pro Leu Lys Arg Glu Leu Glu Asn Leu Lys Ala Lys Leu	
650 655 660	
gct cag cac gtc aaa cca gag gaa cat gag cag ctc aag agc aga tta	2428
Ala Gln His Val Lys Pro Glu Glu His Glu Gln Leu Lys Ser Arg Leu	
665 670 675	
gag cag aag tca gga gaa ctt ggg aag agg atc act gag tta aca tcg	2476
Glu Gln Lys Ser Gly Glu Leu Gly Lys Arg Ile Thr Glu Leu Thr Ser	
680 685 690 695	
aaa aat cag acg tta caa aag gaa atc gaa aag gtc tgc ctg gat aat	2524
Lys Asn Gln Thr Leu Gln Lys Glu Ile Glu Lys Val Cys Leu Asp Asn	
700 705 710	
aag ctc ctt aca caa caa gta aat aac tta aca act gaa atg aaa aat	2572
Lys Leu Leu Thr Gln Gln Val Asn Asn Leu Thr Thr Glu Met Lys Asn	
715 720 725	
cat tac gtc cct tta aaa gta agt gaa gaa atg aaa aag tca cat gat	2620
His Tyr Val Pro Leu Lys Val Ser Glu Glu Met Lys Lys Ser His Asp	
730 735 740	
gta att gtt gat gat ttg aat aaa aag ctt tca gat gtg aca cac aaa	2668
Val Ile Val Asp Asp Leu Asn Lys Lys Leu Ser Asp Val Thr His Lys	
745 750 755	
tat aca gaa aag aag ttg gaa atg gag aag ttg ctt atg gaa aat gcc	2716
Tyr Thr Glu Lys Lys Leu Glu Met Glu Lys Leu Leu Met Glu Asn Ala	
760 765 770 775	

### Figure 4-5

agt tta agt aaa aat gtc agc cgc ctg gaa act gtg ttc ata cct ccc Ser Leu Ser Lys Asn Val Ser Arg Leu Glu Thr Val Phe Ile Pro Pro	2764
780 785 790	
gag aga cac gaa aaa gaa atg atg gct ctg aaa tcc aat atc act gaa Glu Arg His Glu Lys Glu Met Met Ala Leu Lys Ser Asn Ile Thr Glu	2812
795 800 805	
ctt aag aag cag ctg tct gaa ctt aat aaa aaa tgt ggt gaa gac caa Leu Lys Lys Gln Leu Ser Glu Leu Asn Lys Lys Cys Gly Glu Asp Gln	2860
810 815 820	
gag aaa ata tat tca ctc atg tct gaa aac aat gat ttg aaa aag acc Glu Lys Ile Tyr Ser Leu Met Ser Glu Asn Asn Asp Leu Lys Lys Thr	2908
825 830 835	
atg agt cat cag tat gtg ccc gtg aaa acc cat gaa gag att aaa act Met Ser His Gln Tyr Val Pro Val Lys Thr His Glu Glu Ile Lys Thr	2956
840 845 850 855	
gcc ttg agt agc aca ttg gat aaa acc aat aga gaa tta gta gat gtg Ala Leu Ser Ser Thr Leu Asp Lys Thr Asn Arg Glu Leu Val Asp Val	3004
860 865 870	
aag aag aag tgt gaa gat ata aat caa gaa ttt gtg aaa ata aaa gat Lys Lys Lys Cys Glu Asp Ile Asn Gln Glu Phe Val Lys Ile Lys Asp	3052
875 880 885	
gag aac gaa ata tta aaa aga aat ctg gag aac act cag aac caa gta Glu Asn Glu Ile Leu Lys Arg Asn Leu Glu Asn Thr Gln Asn Gln Val	3100
890 895 900	
aaa gct gag tac atc agc cta aga gag cat gaa gaa aag atg agt ggc Lys Ala Glu Tyr Ile Ser Leu Arg Glu His Glu Glu Lys Met Ser Gly	3148
905 910 915	
cta agg aag agc atg aag aag gtc cag gac aac agc gct gaa ata ctg Leu Arg Lys Ser Met Lys Lys Val Gln Asp Asn Ser Ala Glu Ile Leu	3196
920 925 930 935	
gct aag tac aaa aaa agc cag gag gag att gtc acc ctg cat gag gag Ala Lys Tyr Lys Lys Ser Gln Glu Glu Ile Val Thr Leu His Glu Glu	3244
940 945 950	
att gca gcc cag aag aga gaa ctc gac acg ata cag gaa tgc atc aag Ile Ala Ala Gln Lys Arg Glu Leu Asp Thr Ile Gln Glu Cys Ile Lys	3292
955 960 965	
cta aaa tat gct ccg atc atc agc ttg gaa gag tgt gag aga aaa ttt Leu Lys Tyr Ala Pro Ile Ile Ser Leu Glu Glu Cys Glu Arg Lys Phe	3340
970 975 980	

Figure 4-6

aaa gcc act gag aaa gaa cta aaa gaa cag cta tcc cag cag aca cag Lys Ala Thr Glu Lys Glu Leu Lys Glu Gln Leu Ser Gln Gln Thr Gln 985 990 995	3388
aag tat aat acc agt gaa gaa gag gcc aag aag tgc aag caa gag aat Lys Tyr Asn Thr Ser Glu Glu Glu Ala Lys Lys Cys Lys Gln Glu Asn 1000 1005 1010 1015	3436
gac aag tta aag aag gag atc ctc act ctt cag aag gat cta aag gat Asp Lys Leu Lys Lys Glu Ile Leu Thr Leu Gln Lys Asp Leu Lys Asp 1020 1025 1030	3484
aag aat gtt cac att gag aat tct tat gaa aca gaa aga gca tta agc Lys Asn Val His Ile Glu Asn Ser Tyr Glu Thr Glu Arg Ala Leu Ser 1035 1040 1045	3532
aga aaa aca gaa gag ctg aac aga cag tta aaa gac ctg ttg cag aaa Arg Lys Thr Glu Glu Leu Asn Arg Gln Leu Lys Asp Leu Leu Gln Lys 1050 1055 1060	3580
tac aca gag gca aag aag gag aaa gag aag ctc gtg gag gaa aat gcc Tyr Thr Glu Ala Lys Lys Glu Lys Glu Lys Leu Val Glu Glu Asn Ala 1065 1070 1075	3628
aag cag act tct gag atc ctt gca gca caa act ctt ttg cag aag cag Lys Gln Thr Ser Glu Ile Leu Ala Ala Gln Thr Leu Leu Gln Lys Gln 1080 1085 1090 1095	3676
cat gtt ccg ctg gag cag gtt gag tcc ctg aaa aaa tct ctt agt ggt His Val Pro Leu Glu Gln Val Glu Ser Leu Lys Lys Ser Leu Ser Gly 1100 1105 1110	3724
aca atc gag aca ctc aag gaa gaa ctg aaa act aag cag aga tgt tat Thr Ile Glu Thr Leu Lys Glu Glu Leu Lys Thr Lys Gln Arg Cys Tyr 1115 1120 1125	3772
gag aaa gag cag cag aca gtg acc caa ctg cgg cag atg ctg gag aat Glu Lys Glu Gln Gln Thr Val Thr Gln Leu Arg Gln Met Leu Glu Asn 1130 1135 1140	3820
cag aag aac tcc tct gtg ccc ctg gct gag cat ttg cag gtt aag gaa Gln Lys Asn Ser Ser Val Pro Leu Ala Glu His Leu Gln Val Lys Glu 1145 1150 1155	3868
gca ttt gag aaa gaa gtt gga atc ata aaa gct agc ttg aga gaa aag Ala Phe Glu Lys Glu Val Gly Ile Ile Lys Ala Ser Leu Arg Glu Lys 1160 1165 1170 1175	3916
gaa gaa gaa agc caa aac aaa act gaa gag gtc tcc aaa ctc cag tct Glu Glu Glu Ser Gln Asn Lys Thr Glu Glu Val Ser Lys Leu Gln Ser 1180 1185 1190	3964

Figure 4-7

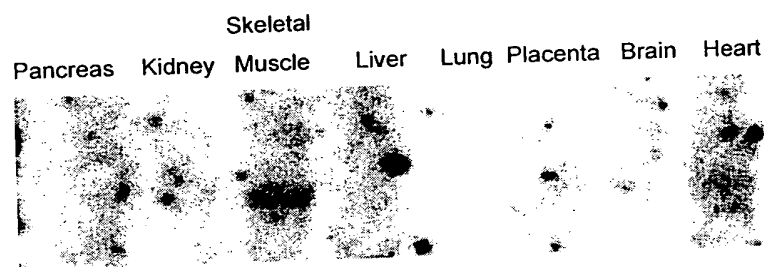
gag att cag aat act aaa caa gcg tta aaa aaa tta gag act cgg gag Glu Ile Gln Asn Thr Lys Gln Ala Leu Lys Lys Leu Glu Thr Arg Glu 1195 1200 1205	4012
gtg gtt gat ttg tgc aaa tat aaa gca acg aaa agc gat ttg gag aca Val Val Asp Leu Ser Lys Tyr Lys Ala Thr Lys Ser Asp Leu Glu Thr 1210 1215 1220	4060
cag att tcc gac tta aac gaa aaa ttg gcc aat ctg aat agg aag tat Gln Ile Ser Asp Leu Asn Glu Lys Leu Ala Asn Leu Asn Arg Lys Tyr 1225 1230 1235	4108
gag gaa gta tgt gag gag gtt ttg cat gcc aaa aag aag gaa ctg tct Glu Glu Val Cys Glu Glu Val Leu His Ala Lys Lys Lys Glu Leu Ser 1240 1245 1250 1255	4156
gct aaa gat gag aag gaa ttg ctc cat ttc agc ata gag caa gaa atc Ala Lys Asp Glu Lys Glu Leu Leu His Phe Ser Ile Glu Gln Glu Ile 1260 1265 1270	4204
aaa gat cag cag gaa cga tgt gac aaa tcc tta aca acc atc acg gag Lys Asp Gln Gln Glu Arg Cys Asp Lys Ser Leu Thr Thr Ile Thr Glu 1275 1280 1285	4252
cta cag aga aga ata cag gaa tct gcc aaa caa atc gaa gca aaa gat Leu Gln Arg Arg Ile Gln Glu Ser Ala Lys Gln Ile Glu Ala Lys Asp 1290 1295 1300	4300
aat aag ata act gaa ctg ctc aat gat gtg gag aga tta aaa cag gcc Asn Lys Ile Thr Glu Leu Leu Asn Asp Val Glu Arg Leu Lys Gln Ala 1305 1310 1315	4348
ctc aat ggc ctt tcc cag ctc acc tat gga agt ggg agt ccc agc aag Leu Asn Gly Leu Ser Gln Leu Thr Tyr Gly Ser Gly Ser Pro Ser Lys 1320 1325 1330 1335	4396
agg cag agt cag ctg att gac agc ctg cag cag cag gtc agg tcc ctg Arg Gln Ser Gln Leu Ile Asp Ser Leu Gln Gln Gln Val Arg Ser Leu 1340 1345 1350	4444
cag cag cag ctg gcg gat gcc gac aga cag cac caa gaa gta att gca Gln Gln Gln Leu Ala Asp Ala Asp Arg Gln His Gln Glu Val Ile Ala 1355 1360 1365	4492
att tat cgg aca cac ctt ctt agt gct gca cag ggt cac atg gat gag Ile Tyr Arg Thr His Leu Leu Ser Ala Ala Gln Gly His Met Asp Glu 1370 1375 1380	4540
gat gtg cag gcc gcc tta ctg cag atc ata cag atg cgg cag ggg ctc Asp Val Gln Ala Ala Leu Leu Gln Ile Ile Gln Met Arg Gln Gly Leu 1385 1390 1395	4588

# Figure 4-8

gtg tgc tagtcggcac cccccagccc acagtggcctt tccttgctgg tgctgagcat 4644  
Val Cys  
1400  
tctgtgcgca acttcatggc ctttctgggc ctgctgtgc tagtataatt aaaataaagt 4704  
gtattttgat ccatcaaaaa aaaaaaaaaa aa 4736

gtg tgc tagtcggcac cccccagccc acagtggcctt tccttgctgg tgctgagcat 4644  
Val Cys  
1400  
tctgtgcgca acttcatggc ctttctgggc ctgctgtgc tagtataatt aaaataaagt 4704  
gtattttgat ccatcaaaaa aaaaaaaaaa aa 4736

**Figure 5**



Bcap73 mRNA is expressed in various human tissues

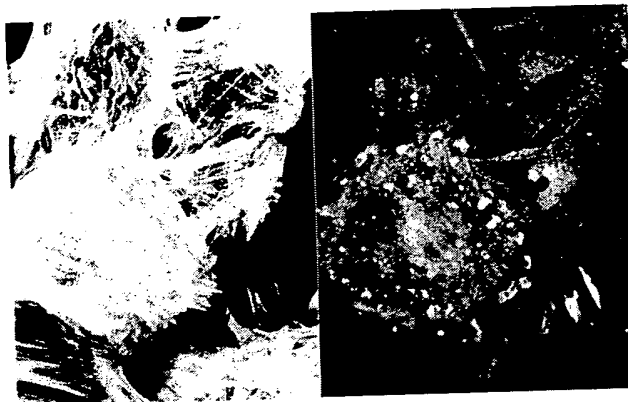
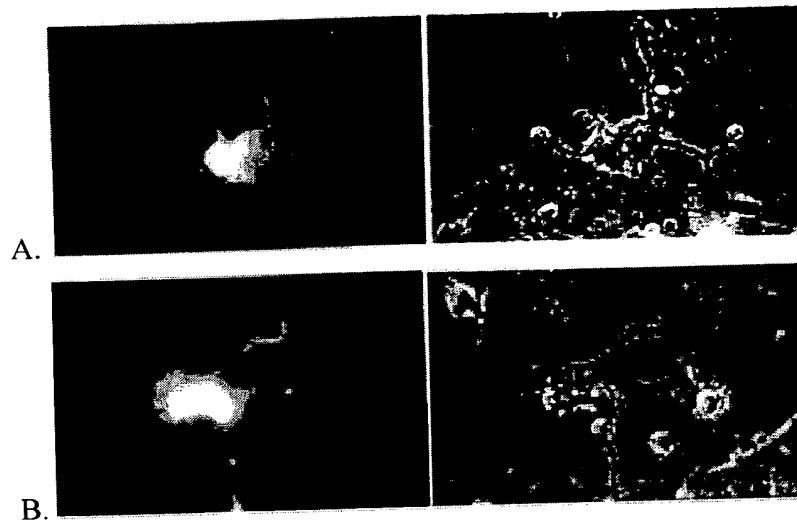
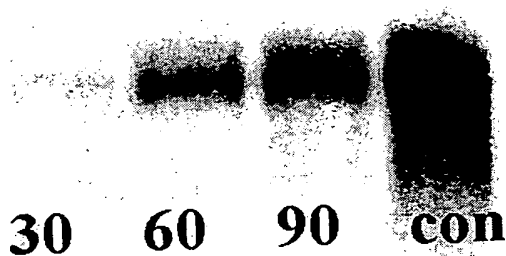
[illegible]

Figure 7



Overexpression of bcap73 domains induces aberrant cellular projections

**Figure 8**



Bcap73 mRNA is down-regulated in response to injury

Figure 8 shows a Northern blot analysis of Bcap73 mRNA levels in response to injury. The blot displays four lanes labeled 30, 60, 90, and con. The 30, 60, and 90 lanes represent time points post-injury, while the con lane represents the control. The bands for 60 and 90 minutes are significantly darker than the control, indicating down-regulation of Bcap73 mRNA in response to injury.

### Figure 9-1

Sequence Alignment of bcap73 cDNA against Canine familiaris mRNA for C3VS protein  
(GenBank accession X99145)

Query= $\beta$ CAP73

Sbjct=C3VS

```

Query: 358 tttgctgtagcaacaagaaactaaatcctgtctatgatgagctgttggttttcttgtgc 417
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 12 tttgctgtagcaaccagaaaccaaactcctgtctatgatgaactgttggttttcttgtgc 71

```

```
Query: 418 tcctaagaacagacaagcagcagattggaacaaatcgatgccgattgatgagagcgc 477
          ||| ||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||| |||
Sbjct: 72 tccaagaacagacatgcagcagattggaacaaatatgatgccgattgatgaaagccgc 131
```

[illegible]

```
Query: 538 caagctagatgtagaaggcagatctgcctttcatgttggtggcctcaaagggaaatcttga 597  
      ||| ||||| | | ||||||| ||||||| ||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 192 caaac tagatgtggaaggcagatctgcctccatgttggtggcctcaaaggggaatcttga 251
```

```

Query: 598  gtgtttgaatgccatcctcatacatggagttgatattacaaccagtgacaccgcaggaag 657
           |||
Sbjct: 252  atgtttgaatgccatccttatacatggagttgatattacaaccagtgacactgcaggaag 311

```

```

Query: 658  gaatgctcttcacctggctgcaaagtatgggcatgcactgtgtctacaaaaacttctaca 717
           |||
Sbjct: 312  aaatgctcttcacttggctgcaaagtatgggcatgcattgtgtctacaaaaacttctaca 371

```

```

Query: 718  gtacaattgtcccaactgaacatgtagacctgcaggaagaactgcacttcatgatgcagc 777
            |||
Sbjct: 372  gtacaattgtcccaactgaacatgcagacctgcaggaagaaccgcacttcatgacgcagc 431

```

```

Query: 778  tatggcagactgtccttctagcatcacagctgctctgcgaccatggggcctcggtgaatgc 837
           |||
Sbjct: 432  aatggcagactgtccttccagcatcacagctgctttgtgaccatggggcctccgtgaatgc 491

```

```

Query: 838   caaagatgtagatgggcggaaccacttggtctgggtaccagatgtgtaggccacaat 897
            |||
Sbjct: 492   caaagatgtggatgggcggaaccgctgggtctgggtactcagatgtgtaggccagcaat 551

```

[illegible]

Figure 9-2

Query: 898 atgtcaactgctgatagatagaggggcgatattaattccagagacaaacaaaacaggac 957  
 |||||||||||||||| ||||| || |||||||||||||||||||||  
 Sbjct: 552 ctgtcaactgctgatagatcgaggggcagagattaattccagagacaaacaaaacagaac 611

Query: 958 tgctctcatgctaggatgcgagtatgggttgcaaagatgcagtagaagtcttaataaaaa 1017  
 |||||||||||| || |||||||||||||||| || ||||| |||||||||||||  
 Sbjct: 612 tgctctcatgcttgggttgcgagtatgggttgtaaggatgctgtagaagtcttacttaaaaa 671

Query: 1018 cggcgctgacgtgaccttgctggacgccttgggccatgacagttcttactatgcaagaat 1077  
 || ||||| || || ||||| ||||| ||||| ||||||||| |||||||||  
 Sbjct: 672 tgggtgctgatgtaagcctgctggatgccttggggccatgatagttcttactatgcaagaat 731

Query: 1078 tggtgacaatctggacattctaacccttactgaagactgcatcagaaaattccaacaaagg 1137  
 |||||||||||||||| || ||||||||||||| ||||||||| |||||||||  
 Sbjct: 732 tggtgacaatctggacattctaactttattgaagactgcgtcagaaaataccaacaaagg 791

Query: 1138 gagagaactttggaagaaaggaccatctttacaacagcgaaatttgctcagatgctaga 1197  
 |||||||||||||||| ||||||||||||| ||||||||| || |||||||||  
 Sbjct: 792 gagagaactttggaagaaaggaccatctttacagcagcgaaatttgccgtacatgctaga 851

Query: 1198 tgaagtaaatacgaagtcaaatacagagggagcatcaaacattcaggatctggagattga 1257  
 ||||||||| ||||||||| ||||||||||||| ||||||||| |||||||||  
 Sbjct: 852 tgaagtaaattgtgaagtcaagtcagagggagcatcgaaacattcaggagctggagattga 911

Query: 1258 aaatgaagatctgaaagagagattgagaaaaattcagcaagaacagagaatattattgga 1317  
 ||||||||| ||||||||| ||||||||||||| ||||||||| |||||||||  
 Sbjct: 912 aaatgaagatttgaaagacagggttgagaaaaattcagcaagaacagagaatattactgga 971

Query: 1318 taaagtcaatgggtttacagctacagctgaatgaggaagtaatgggtggctgatgatctgga 1377  
 ||||||||||||| ||||||||||||| ||||||||| ||||| |||||||||  
 Sbjct: 972 taaagtcaatgggtttacaactacagctgaatgaggaagtgatgggtgctgatgatctgga 1031

Query: 1378 aagtgagaaagaaaagctgaagtccttttggcagccaaagaaaagcagcatgaagaaag 1437  
 |||||||||||||||| ||||||| || ||||||||| |||||||||  
 Sbjct: 1032 aagtgagaaagaaaagctgaagtccttttgggtggctaaagaaaagcaacatgaagaaag 1091

Query: 1438 cctaagaactattgaggctctgaaaagtagatttaagtattttgag 1483  
 ||||||||||||| ||||||||| ||||||||| |||||||||  
 Sbjct: 1092 cctaagaactattgagtcctctgaaaaacagatttaaatattttgag 1137

Figure 9-3

Query: 1566 agtgtacttccacaggcatgccagtcctatgcaaagccgatctatgttaagaccactgg 1625  
|||||  
Sbjct: 1136 agtgtacttccccaggggtgccagcccacatgcaaagcaggtctatgttaagaccactgg 1195

Query: 1626 agctagccttacctaatacaagcctcatattcggaacgaaattttaagaaagaattag 1685  
|||||  
Sbjct: 1196 agctatcattacccaatcaaacctcatattctgaaaatgacctcttaagaaagagttag 1255

Query: 1686 aagcaatgagaactttctgtgattcagcaaaacaagacagactcaaactccaaaatgaac 1745  
|||||  
Sbjct: 1256 aagcaatgagaactttctgcgaatcagccaaacaagaccgctcaagctccagaacggag 1315

Query: 1746 tggctcacaaggtggcggagtgcaggccttagcattggaatgtgaaaggggtgaaagagg 1805  
|||||  
Sbjct: 1316 tggcgcacaaggtggctgagtgcaggcttaggactagaatgtgaacgcacatcaaggagg 1375

Query: 1806 attcagatgagcagataaagcaactagaagatgccttgaaagacgtgcagaagagaatgt 1865  
|  
Sbjct: 1376 actctgatgagcagataaagcagttagaagacgcattgaaagatgtgcagaagagaatgt 1435

Query: 1866 atgagtcggaaggtaaagtgaacaaatgcagacacattttcttgccttgaaagagcacc 1925  
|||||  
Sbjct: 1436 atgagtcggaaggtaaagtaaaacaaatgcagacacactttcttgccttgaaagagcacc 1495

Query: 1926 tgacaagtgatgcggccactgggaaccacaggctgatggaggaaactgaaggatcagttga 1985  
|||||  
Sbjct: 1496 tgaccagtgaagcagctataggggaatcacagactaatggaggagctgaaggatcagttga 1555

Query: 1986 aagacatgaaagtgaatacgaaggtgcgtccgcagaagtggggaattgagaaaccaa 2045  
|  
Sbjct: 1556 aggacatgaaagcgaaatatgaggggtgcatcagcagaagtgggaaaactgcgaaccaa 1615

Query: 2046 tcaaacaaaatgaaatgttagttgaagagtttaagagagatgagggcaagctgatggaag 2105  
|||||  
Sbjct: 1616 tcaaacaaaatgagctgctagtagaacagtttaggagagatgaaggcaagctggtggaag 1675

Query: 2106 agaataagcgactgcagaaggagttgagcatgtgtgaactggagcgagagaagagaggaa 2165  
|||||  
Sbjct: 1676 agaataagcgattgcagaaggaaactcagtatgtgtgaaacggagcgagacaagaaaggaa 1735

Figure 9-4

Query: 2166 ggaagctcactgagatggaaggccaggttaaaggacttgctcagccaagctggccctttcta 2225  
||| | | ||||| ||||| ||||| ||||| | | ||| ||||| || | |  
Sbjct: 1736 ggagggttgctgaggtggaaggccaggttaaaggaactcttagcaaagctgaccttgctcag 1795

Query: 2226 ttccagcagagaaatttgaaaacatgaagagcttggttatcaa 2267  
||||| | | ||||| | ||||| ||||| |||||  
Sbjct: 1796 ttccaactgaaaaatttgagagcatgaagagcttattatcaa 1837

Query: 1796 ttccaactgaaaaatttgagagcatgaagagcttattatcaa 1837  
Sbjct: 2226 ttccagcagagaaatttgaaaacatgaagagcttggttatcaa 2267

Figure 10-1

Sequence Alignment of bcap73 against Tentative Human Concensus (THC) Contiguous Sequences  
THC244788 THC143090 THC186491 THC213238 (from TIGR)

Score = 1052 bits (547), Expect = 0.0  
Identities = 905/1092 (82%), Positives = 905/1092 (82%), Gaps = 4/1092 (0%)

Query=bcap73 cDNA  
Sbjct=THC seq

Query: 3136 aaagatgagtggcctaaggaagagcatgaagaaggtccaggacaacagcgctgaaatact 3195  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 6 aaagatgagctcgctaagtcagagcatgagaaaggtscaggatagtaatgctgaaatctt 65

Query: 3196 ggctaagtacnnnnnnngccaggaggagattgtcaccctgcatgaggagattgcagccca 3255  
||| | ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 66 ggccamctacagaaaaggccaagaagagattgtgacactkcatgccgaaattaragccca 125

Query: 3256 gaagagagaactcgacacgatacaggaatgcatcaagctaaaatatgctccgatcatcag 3315  
|| || || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 126 gargarggagctcgacacaatacaagartgcattaaggtaaaatatgcccccaattgtcag 185

Query: 3316 cttggaagagtgtgagagaaaaatttaaagccactgagaaaagaac-taaaagaacagctat 3374  
||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 186 ctttgaggagtscgagagaaaaatttaaagcaacagagaaaagaacctaaaagaccagttat 245

Query: 3375 cccagcagacacagaagtataataccagtgaagaagaggccaagaagtgcagcaagaga 3434  
| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 246 cagagcagacacaaaagtatagtgtcagtgaagaagaagtcaagaaaaacaagcaagaga 305

Query: 3435 atgacaagttaaagaaggagatcctcactcttcagaaggatctaaaggataagaatgttc 3494  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 306 atgacaagttaaagaaggagattttacccttcagaaagatttgagagayaagacagttc 365

Query: 3495 acattgagaattcttatgaaacagaaagagcattaagcagaaaaacagaagagctgaaca 3554  
||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 366 tcattgagaagtctcatgaaatggaaagagcattaagcagaaaaacagacgagctaaaca 425

Query: 3555 gacagttaaaagacctgttgcaaaatacacagaggcaaaagaaggagaaagagaagctcg 3614  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 426 aacagttaaaagacttgtcacagaaatacacggaagttaaagaatgtgaaagagaagctag 485

### Figure 10-2

[illegible]

**Figure 10-3**

Query: 4215 aggaacgatgtg 4226  
          |||||||  
Sbjct: 1083 aggaacgatgtg 1094

Query: 4215 aggaacgatgtg 4226  
Sbjct: 1083 aggaacgatgtg 1094